

# Block-bootstrap procedure

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 An abbreviated version of this protocol was published in eLIFE in Aug 2018

Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences

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## Detailed protocol

All the scripts used are available on Dryad. <https://datadryad.org/stash/dataset/doi:10.5061/dryad.t76fk80>

I used R to do the blockbootstrap strategy (there is a source code to estimate them):

### confidence Intervals

The blockbootstrapped SFS to make demographic inferences are computed using the functions matsplitter and booti from SFS\_bootstrap.R

If you want to estimate confidence intervals of the SFS you will have to use the functions matsplitter as well as booti.2pop or booti.allpop

And the demographic inferences files are these ones :

### Supplementary file - settings files for demographic inferences

**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Pouyet, F. (2020). Block-bootstrap procedure. Bio-protocol Preprint. [bio-protocol.org/prep409](https://bio-protocol.org/prep409).
2. Pouyet, F., Aeschbacher, S., Thiéry, A. and Excoffier, L. (2018). Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. eLIFE. DOI: [10.7554/eLife.36317](https://doi.org/10.7554/eLife.36317)

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